RAW SEQUENCE LISTING ERROR REPORT

**BIOTECHNOLOGY
SYSTEMS
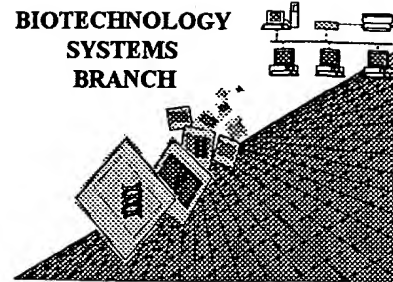BRANCH**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: _09/234,208_

Art Unit / Team No. : _0118_

Date Processed by STIC: _1/29/99_

THE ATTACHED PRINTOUT EXPLAINS THE **ERRORS DETECTED.**

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

ARTI SHAH 703-308-4212

SEQUENCE LISTING
(1) GENERAL INFORMATION:

   (i) APPLICANTS: Clinton, Gail and Doherty, Joni Kristin

   (ii) TITLE OF INVENTION: HER-2 BINDING ANTAGONISTS

   (iii) NUMBER OF SEQUENCES: 9

   (iv) CORRESPONDENCE ADDRESS:
      (A) ADDRESSEE: DAVIS WRIGHT TREMAINE
      (B) STREET: 1501 Fourth Avenue, 2600 Century Square
      (C) CITY: Seattle
      (D) STATE: Washington
      (E) COUNTRY: U.S.A.
      (F) ZIP: 98101

   (v) COMPUTER READABLE FORM:
      (A) MEDIUM TYPE: Floppy disk
      (B) COMPUTER: PC compatible
      (C) OPERATING SYSTEM: Windows95
      (D) SOFTWARE: Word

   (vi) CURRENT APPLICATION DATA:
      (A) APPLICATION NUMBER: to be assigned
      (B) FILING DATE: 20 January 1999
      (C) CLASSIFICATION:

   (viii) ATTORNEY/AGENT INFORMATION:
      (A) NAME: Oster, Jeffrey B.
      (B) REGISTRATION NUMBER: 32,585
      (C) REFERENCE/DOCKET NUMBER: OHSU-1

   (ix) TELECOMMUNICATION INFORMATION:
      (A) TELEPHONE: 206 628 7711
      (B) TELEFAX: 206 628 7699

(2) INFORMATION FOR SEQ ID NO:1:

   (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 79
      (B) TYPE: polypeptide
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: unknown
   (ii) MOLECULE TYPE: HER-2 ECD antagonist
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
Gly Thr His Ser Leu Leu Pro Arg Pro Ala Ala Val Pro Val Pro Leu
              5                  10                 15
Arg Met Gln Pro Gly Pro Ala His Pro Val Leu Ser Phe Leu Arg Pro
             20                  25                 30
Ser Trp Asp Leu Val Ser Ala Phe Tyr Ser Leu Pro Leu Ala Pro Leu
        35                  40                  45
Ser Pro Thr Ser Val Pro Ile Ser Pro Val Ser Val Gly Arg Gly Pro
     50                  55                  60
Asp Pro Asp Ala His Val Ala Val Asn Leu Ser Arg Tyr Glu Gly
65                  70                  75
```

(2) INFORMATION FOR SEQ ID NO:2:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 419
       (B) TYPE: protein *amino acid*
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: unknown
    (ii) MOLECULE TYPE: polypeptide
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Met Glu Leu Ala Ala Leu Cys Arg Trp Gly Leu Leu Leu Ala Leu Leu
                5                  10                  15
Pro Pro Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr Asp Met Lys
               20                  25                  30
Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His
           35                  40                  45
Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr
           50                  55                  60
Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val
       65                  70                  75
Gln Gly Tyr Val Leu Ile Ala His Asn Gln Val Arg Gln Val Pro Leu
80                  85                  90                      95
Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr
               100                 105                 110
Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn Thr Thr Pro
           115                 120                 125
Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln Leu Arg Ser
           130                 135                 140
Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Gln Arg Asn Pro Gln
       145                 150                 155
Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn
160                 165                 170                 175
Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser Arg Ala Cys
               180                 185                 190
His Pro Cys Ser Pro Met Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser
               195                 200                 205
Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys
           210                 215                 220
Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His Glu Gln Cys
       225                 230                 235
Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu Ala Cys Leu
240                 245                 250                 255
His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro Ala Leu Val
               260                 265                 270
Thr Tyr Asn Thr Asp Thr Phe Glu Ser Met Pro Asn Pro Glu Gly Arg
           275                 280                 285
Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr Asn Tyr Leu
           290                 295                 300
Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu His Asn Gln
       305                 310                 315
Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser Lys
320                 325                 330                 335
Pro Cys Ala Arg Gly Thr His Ser Leu Leu Pro Arg Pro Ala Ala
               340                 345                 350
Val Pro Val Pro Leu Arg Met Gln Pro Gly Pro Ala His Pro Val Leu
               355                 360                 365
```

```
Ser Phe Leu Arg Pro Ser Trp Asp Leu Val Ser Ala Phe Tyr Ser Leu
        370                 375             380
Pro Leu Ala Pro Leu Ser Pro Thr Ser Val Pro Ile Ser Pro Val Ser
        385                 390             395
Val Gly Arg Gly Pro Asp Pro Asp Ala His Val Ala Val Asn Leu Ser
400                 405             410                 415
Arg Tyr Glu Gly  419
```

(2) INFORMATION FOR SEQ ID NO:3:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 19
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: unknown
        (ii) MOLECULE TYPE: oligonucleotide
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

    TGAGCACCAT GGAGCTGGC 19

(2) INFORMATION FOR SEQ ID NO:4:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 22
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: unknown
        (ii) MOLECULE TYPE: oligonucleotide
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TCCGGCAGAA ATGCCAGGCT CC 22

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(2) INFORMATION FOR SEQ ID NO:5:
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 22
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: unknown
        (ii) MOLECULE TYPE: oligonucleotide
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AACACAGCGG TGTGAGAAGT GC 22

(2) INFORMATION FOR SEQ ID NO:6:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 21
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: unknown
        (ii) MOLECULE TYPE: oligonucleotide
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATACCGGGAC AGGTCAACAG C 21

hard return

(2) INFORMATION FOR SEQ ID NO:7:   (i) SEQUENCE CHARACTERISTICS: (A)
LENGTH: 20   (B) TYPE: nucleic acid   (C) STRANDEDNESS: single
(D) TOPOLOGY: unknown   (ii) MOLECULE TYPE: oligonucleotide

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TCTGGGTACC CACTCACTGC 20

hand return

(2) INFORMATION FOR SEQ ID NO:8: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown
    (ii) MOLECULE TYPE: oligonucleotide
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TTCACACTGG CACGTCCAGA CC 22

(2) INFORMATION FOR SEQ ID NO:9: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: unknown
    (ii) MOLECULE TYPE: oligonucleotide
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCACGGATCC ATAGCAGACT GAGGAGG 27

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